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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/053,192

DATE: 02/12/2002
TIME: 15:34:11

Input Set : A:\20347us1.app
Output Set: N:\CRF3\02122002\J053192.raw

ENTERED

<110> APPLICANT: BACHMANN, Heinrich
BRUGGER, Roland
FRIEDLEIN, Arno M
WIRTZ, Gabriele M
WOGGON, Wolf-Dietrich
WYSS, Adrian
WYSS, Markus
<120> TITLE OF INVENTION: BETA,BETA-CAROTENE 15,15'-DIOXYGENASES, NUCLEIC ACID SEQUENCES CODING THEREFOR AND THEIR USE
<130> FILE REFERENCE: B,B-CAROTENE 15,15'-DIOXYGENASES,...
C--> <140> CURRENT APPLICATION NUMBER: US/10/053,192
C--> <141> CURRENT FILING DATE: 2002-01-15
<150> PRIOR APPLICATION NUMBER: 103382.0
<151> PRIOR FILING DATE: 1999-02-22
<160> NUMBER OF SEQ ID NOS: 10
<170> SOFTWARE: PatentIn Ver. 2.1
<210> SEQ ID NO: 1
<211> LENGTH: 526
<212> TYPE: PRT
<213> ORGANISM: CHICKEN
<400> SEQUENCE: 1

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            20                  25                  30
Leu Arg Asn Gly Pro Gly Met His Thr Ile Gly Asp Thr Lys Tyr Asn
        35                  40                  45
His Trp Phe Asp Gly Leu Ala Leu Leu His Ser Phe Thr Phe Lys Asn
    50                  55                  60
Gly Glu Val Tyr Tyr Arg Ser Lys Tyr Leu Arg Ser Asp Thr Tyr Asn
65                  70                  75                  80
Cys Asn Ile Glu Ala Asn Arg Ile Val Val Ser Glu Phe Gly Thr Met
                85                  90                  95
Ala Tyr Pro Asp Pro Cys Lys Asn Ile Phe Ala Lys Ala Phe Ser Tyr
            100                 105                 110
Leu Ser His Thr Ile Pro Glu Phe Thr Asp Asn Cys Leu Ile Asn Ile
        115                 120                 125
Met Lys Thr Gly Asp Asp Tyr Tyr Ala Thr Ser Glu Thr Asn Phe Ile
    130                 135                 140
Arg Lys Ile Asp Pro Gln Thr Leu Glu Thr Leu Asp Lys Val Asp Tyr
145                 150                 155                 160
Ser Lys Tyr Val Ala Val Asn Leu Ala Thr Ser His Pro His Tyr Asp
                165                 170                 175
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65 Ser Ala Gly Asn Ile Leu Asn Met Gly Thr Ser Ile Val Asp Lys Gly
66             180                 185                 190
68 Arg Thr Lys Tyr Val Leu Phe Lys Ile Pro Ser Ser Val Pro Glu Lys
69         195                 200                 205
71 Glu Lys Lys Lys Ser Cys Phe Lys His Leu Glu Val Val Cys Ser Ile
72     210                 215                 220
74 Pro Ser Arg Ser Leu Leu Gln Pro Ser Tyr Tyr His Ser Phe Gly Ile
75 225                 230                 235                 240
77 Thr Glu Asn Tyr Ile Val Phe Ile Glu Gln Pro Phe Lys Leu Asp Ile
78                 245                 250                 255
80 Val Lys Leu Ala Thr Ala Tyr Ile Arg Gly Val Asn Trp Ala Ser Cys
81             260                 265                 270
83 Leu Ser Phe His Lys Glu Asp Lys Thr Trp Phe His Phe Val Asp Arg
84         275                 280                 285
86 Lys Thr Lys Lys Glu Val Ser Thr Lys Phe Tyr Thr Asp Ala Leu Val
87     290                 295                 300
89 Leu Tyr His His Ile Asn Ala Tyr Glu Glu Asp Gly His Val Val Phe
90 305                 310                 315                 320
92 Asp Ile Val Ala Tyr Arg Asp Asn Ser Leu Tyr Asp Met Phe Tyr Leu
93                 325                 330                 335
95 Lys Lys Leu Asp Lys Asp Phe Glu Val Asn Asn Lys Leu Thr Ser Ile
96             340                 345                 350
98 Pro Thr Cys Lys Arg Phe Val Val Pro Leu Gln Tyr Asp Lys Asp Ala
99         355                 360                 365
101 Glu Val Gly Ser Asn Leu Val Lys Leu Pro Thr Ser Ala Thr Ala Val
102     370                 375                 380
104 Lys Glu Lys Asp Gly Ser Ile Tyr Cys Gln Pro Glu Ile Leu Cys Glu
105 385                 390                 395                 400
107 Gly Ile Glu Leu Pro Arg Val Asn Tyr Asp Tyr Asn Gly Lys Lys Tyr
108                 405                 410                 415
110 Lys Tyr Val Tyr Ala Thr Glu Val Gln Trp Ser Pro Val Pro Thr Lys
111             420                 425                 430
113 Ile Ala Lys Leu Asn Val Gln Thr Lys Glu Val Leu His Trp Gly Glu
114         435                 440                 445
116 Asp His Cys Trp Pro Ser Glu Pro Ile Phe Val Pro Ser Pro Asp Ala
117     450                 455                 460
119 Arg Glu Glu Asp Glu Gly Val Val Leu Thr Cys Val Val Val Ser Glu
120 465                 470                 475                 480
122 Pro Asn Lys Ala Pro Phe Leu Leu Ile Leu Asp Ala Lys Thr Phe Lys
123                 485                 490                 495
125 Glu Leu Gly Arg Ala Thr Val Asn Val Glu Met His Leu Asp Leu His
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134 <212> TYPE: DNA
135 <213> ORGANISM: CHICKEN
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138 cggatccact agtaacggcc gccagtgtgg tggaatccat ccttctatgt aacaggaaag 60
139 agctgttctt agcccagaga ggagggcacc gtacgcctgc aggagcagct gggtagagga 120
140 cacaggagag cgatggagac aatatttaac agaaacaaag aagagcatcc agagcccata 180
141 aaagctgagg tgcaaggtca gttgcccact tggttgcaag gggtacttct ccgaaatggc 240
142 ccagggatgc acacaatagg ggacactaaa tacaaccact ggtttgatgg cttggctctg 300
143 ctgcacagct tcacgtttaa aaatggtgaa gtttactaca gaagtaagta cctccgaagt 360
144 gacacatacа actgcaatat agaagcaaac cgaatcgtgg tgtctgagtt tggaaccatg 420
145 gcttatccgg atccatgcaa aaacatattt gccaaggcat tctcatactt atctcacacc 480
146 attcctgagt tcacggacaa ctgcctgatc aacattatga aaactgggga tgattattat 540
147 gctaccagtg agactaactt catcagaaaa attgatccac agactctgga gacactagat 600
148 aaggtagact acagcaaata tgtagctgta aacttggcaa cttctcaccc acactatgac 660
149 agtgctggaa atattctcaa catgggtact tcaattgttg ataaagggag aacaaaatat 720
150 gttctcttta agatcccttc ctctgtacca gaaaaagaaa agaagaaatc ttgttttaaa 780
151 cacctggaag tagtatgctc catcccttct cgctccctgc tccaaccaag ctactaccac 840
152 agctttggaa tcacagaaaa ttatattgtg ttcatagagc agccatttaa actggatatt 900
153 gtcaaactgg caactgccta catccgaggt gtgaactggg cttcctgcct ttcctttcat 960
154 aaggaggata agacgtggtt tcactttgta gacagaaaga cgaaaaaaga agtatccacc 1020
155 aagttttaca ctgatgcttt ggtgctttat caccacataa atgcttacga agaagatggc 1080
156 cacgttgttt ttgatatcgt tgcctacaga gacaatagct tgtacgatat gttttacttа 1140
157 aaaaaactgg acaaagactt tgaagtgaac aacaagctta cctccatccc aacctgcaag 1200
158 cgctttgttg tgcctctgca gtatgacaag gatgcagaag taggttctaa tttagtcaaa 1260
159 cttccaactt ccgcaactgc tgtaaaagaa aaagatggca gcatctattg tcaacctgaa 1320
160 atattatgtg aagggataga actgcctcgt gtcaactatg actacaatgg caaaaaatac 1380
161 aagtatgtct atgcaacaga agtccagtgg agcccagttc ctacaaagat tgcaaaactg 1440
162 aatgtccaaa caaaggaagt actgcactgg ggagaagacc actgctggcc ctcagagccc 1500
163 atctttgttc ccagccccga tgcaagagaa gaggatgaag gtgttgtttt gacctgtgtt 1560
164 gtggtgtctg agccaaataa agcacccttc ctactcatct tggatgctaa aacattcaaa 1620
165 gaattgggcc gagccacagt taacgtagaa atgcatctgg acctgcatgg gatgtttata 1680
166 ccacagaatg atttgggggc tgagacggaa taaaacgcta ttgatccgac tacacaaact 1740
167 gagacaactt tctactgaac atgagttaat atcccttta ccattcaaga acaaccatat 1800
168 aacgacacaa aatgactatg tataatctct taaataatag atataatcct tttaaggcac 1860
169 agcgatgagt tttactacag gtaacgatat gcacaactgg catataacta ttccaaaaga 1920
170 agaagaacga tcagtgtttt agaagtgcta atgttgtaca taacggcggc agagggaaca 1980
171 ggagagaaag gtaacgggaa tatttaatag aatatagatt tctgagcaaa tgaagtgcag 2040
172 tatttatggt gtgatgcatg gcatgagtca cataggtctg cagctcatgt atcttttaga 2100
173 gatcgtttca agattgcagc ttgtgatgca agttttctcc agccagaaaa cctcatttta 2160
174 aaccatctgc tactggtaat tcataccaat gcattttctt ggtgctcgat ttacactata 2220
175 accaaagtta agtattacat tcaggtgcta caactttcta atttacaacc gaaacaaaca 2280
176 agcaaacagc acttgctttg ctaataaccc catggtgtat ttttcctttt tatgatgaca 2340
177 aaaccaagta catatggttt tatgtagcat tcaattatac ttcagtgcta ttccatccta 2400
178 atgttataag caatttgtat ttaaatcagt tttccttgag aatatctgac ataacatttt 2460
179 gtgtaatgag atgactatgt tgtctaaaga tgaacaggaa tgtatctttt attagtattg 2520
180 ttaattgtgt tactaatact atgcatatga atgagagcaa tgtatttcta ggagaactca 2580
181 gatatacatt caacaatttc tgtaggtgaa aatgcattta ctgatgaaag ttgaatcgtt 2640
182 aatgagggag aaaactgggt atccatccat ccaactatgt taggtgttca cctggtctgt 2700
183 atgtgacacc acgctgtttg ggtatctctc actttcacat acctgttctc atggtttctg 2760
184 ctactcactg tattttgcag gagagaaaca aaatgaaatc actgtcactt actatcgccc 2820
185 catcacataa gaacaatggg gctttggtga cttgttcatg attacataag atgtttgcag 2880
186 cagagcagca atagaaccaa caccatccac agttcttgct tgctctgtta tgactcccct 2940
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187 tgctgtcttt atggtttgca tgtatgaaga atacactgcc taattctaat gttaaaaagt 3000
188 cactggggtc agatctagag cttaagtaag cagtctgggg ttttcaaatg tttatatgtt 3060
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212              20                  25                  30
214 Ile Gly Asp Thr Lys Tyr Asn His Trp Phe Asp Gly Leu Ala Leu Leu
215          35                  40                  45
217 His Ser Phe Thr Phe Lys Asn Gly Glu Val Tyr Tyr Arg Ser Lys Tyr
218      50                  55                  60
220 Leu Arg Ser Asp Thr Tyr Asn Cys Asn Ile Glu Ala Asn Arg Ile Val
221  65                  70                  75                  80
223 Val Ser Glu Phe Gly Thr Met Ala Tyr Pro Asp Pro Cys Lys Asn Ile
224                  85                  90                  95
226 Phe Ala Lys Ala Phe Ser Tyr Leu Ser His Thr Ile Pro Glu Phe Thr
227             100                 105                 110
229 Asp Asn Cys Leu Ile Asn Ile Met Lys Thr Gly Asp Asp Tyr Tyr Ala
230         115                 120                 125
232 Thr Ser Glu Thr Asn Phe Ile Arg Lys Ile Asp Pro Gln Thr Leu Glu
233     130                 135                 140
235 Thr Leu Asp Lys Val Asp Tyr Ser Lys Tyr Val Ala Val Asn Leu Ala
236 145                 150                 155                 160
238 Thr Ser His Pro His Tyr Asp Ser Ala Gly Asn Ile Leu Asn Met Gly
239                 165                 170                 175
241 Thr Ser Ile Val Asp Lys Gly Arg Thr Lys Tyr Val Leu Phe Lys Ile
242             180                 185                 190
244 Pro Ser Ser Val Pro Glu Lys Glu Lys Lys Lys Ser Cys Phe Lys His
245         195                 200                 205
247 Leu Glu Val Val Cys Ser Ile Pro Ser Arg Ser Leu Leu Gln Pro Ser
248     210                 215                 220
250 Tyr Tyr His Ser Phe Gly Ile Thr Glu Asn Tyr Ile Val Phe Ile Glu
251 225                 230                 235                 240
253 Gln Pro Phe Lys Leu Asp Ile Val Lys Leu Ala Thr Ala Tyr Ile Arg
254                 245                 250                 255
256 Gly Val Asn Trp Ala Ser Cys Leu Ser Phe His Lys Glu Asp Lys Thr
257             260                 265                 270
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259 Trp Phe His Phe Val Asp Arg Lys Thr Lys Lys Glu Val Ser Thr Lys
260         275                 280                 285
262 Phe Tyr Thr Asp Ala Leu Val Leu Tyr His His Ile Asn Ala Tyr Glu
263     290                 295                 300
265 Glu Asp Gly His Val Val Phe Asp Ile Val Ala Tyr Arg Asp Asn Ser
266 305                 310                 315                 320
268 Leu Tyr Asp Met Phe Tyr Leu Lys Lys Leu Asp Lys Asp Phe Glu Val
269                 325                 330                 335
271 Asn Asn Lys Leu Thr Ser Ile Pro Thr Cys Lys Arg Phe Val Val Pro
272             340                 345                 350
274 Leu Gln Tyr Asp Lys Asp Ala Glu Val Gly Ser Asn Leu Val Lys Leu
275         355                 360                 365
277 Pro Thr Ser Ala Thr Ala Val Lys Glu Lys Asp Gly Ser Ile Tyr Cys
278     370                 375                 380
280 Gln Pro Glu Ile Leu Cys Glu Gly Ile Glu Leu Pro Arg Val Asn Tyr
281 385                 390                 395                 400
283 Asp Tyr Asn Gly Lys Lys Tyr Lys Tyr Val Tyr Ala Thr Glu Val Gln
284                 405                 410                 415
286 Trp Ser Pro Val Pro Thr Lys Ile Ala Lys Leu Asn Val Gln Thr Lys
287             420                 425                 430
289 Glu Val Leu His Trp Gly Glu Asp His Cys Trp Pro Ser Glu Pro Ile
290         435                 440                 445
292 Phe Val Pro Ser Pro Asp Ala Arg Glu Glu Asp Glu Gly Val Val Leu
293     450                 455                 460
295 Thr Cys Val Val Val Ser Glu Pro Asn Lys Ala Pro Phe Leu Leu Ile
296 465                 470                 475                 480
298 Leu Asp Ala Lys Thr Phe Lys Glu Leu Gly Arg Ala Thr Val Asn Val
299                 485                 490                 495
301 Glu Met His Leu Asp Leu His Gly Met Phe
302             500                 505
305 <210> SEQ ID NO: 5
306 <211> LENGTH: 529
307 <212> TYPE: PRT
308 <213> ORGANISM: BOVINE
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315              20                  25                  30
317 Phe Glu Val Gly Ser Glu Pro Phe Tyr His Leu Phe Asp Gly Gln Ala
318          35                  40                  45
320 Leu Leu His Lys Phe Asp Phe Lys Glu Gly His Val Thr Tyr His Arg
322      50                  55                  60
323 Arg Phe Ile Arg Thr Asp Ala Tyr Val Arg Ala Met Thr Glu Lys Arg
324  65                  70                  75                  80
326 Ile Val Ile Thr Glu Phe Gly Phe Thr Thr Cys Ala Phe Pro Asp Pro
327                 85                  90                  95
329 Cys Lys Asn Ile Phe Ser Arg Phe Phe Ser Tyr Phe Arg Gly Val Glu
330             100                 105                 110
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VERIFICATION SUMMARY DATE: 02/12/2002
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L:16 M:270 C: Current Application Number differs, Replaced Application Number
L:17 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:454 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:476 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9